

#4

humPMS2	(2574)	2661	CAATTCTCAGGAC-----	2730
AtPMS2	(2267)	2731	CTTACCTGATGACGACAATGTCAATGATGATGATGATGATGCAACCATCTCATGGC	
Consensus	(2661)		C TT CTCA A	
humPMS2	(2587)	2731	----	
AtPMS2	(2337)		ATGA	
Consensus	(2731)			

FIG. 1

FIG. 1







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humPMS2 (1) -----VERAESSS-----EPAKAKPIIDRKSCHOCSSQVLSLSTAVKELVENSLSAGATNIDL
AtMLH1 (1) MIDDSSLTAPVEEESPAITIVPREPPKORLEESVNRFAAEPIQRPVSAVKELVENSLSDDSSSSSV
Consensus (1) ME ES AT I ID V I AG VI SAVKELVENSLSDA AS I L

71 140
humPMS2 (57) KLAAYVLEHEVSENECQVEEENFECLTLKHHSIQEFAETQVETFFEGEELSSLCALSDVVISCH
AtMLH1 (71) VVPCSLKQVNSDCHIRRDLPICERTISDLTKEDPFLSSMGPRGEALASTYVAHVVTIT
Consensus (71) LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST

141 210
humPMS2 (127) ASAKVCTILMFDHNGKIIQKTPYPRPRCTIVSQQCESTLPVHEEFRIKKETAPMGOVHAYCISA
AtMLH1 (141) KQQIHCVSYRDGVMEHEPKACAAYKQIIMGENSYNMIAETITLSSADDCGRTDLSRMACHYN
Consensus (141) G RL F KGT I V NLF L R K Q N DYAKIV LL I

211 280
humPMS2 (197) GIRVSCINQLGCKKQRPVCTGGSSPIKENGGVFPQKQLQSIPFVOLPPSDSVCEEYGLSCSALHNL
AtMLH1 (210) NVSPFCRKH---SAVKADHSVVSERLDSERGVSVSAKNM---KV---E-----VSSCSSGCT
Consensus (211) I SC G V S SPS D I SVFG LI L LS DA

281 350
humPMS2 (267) EYISSEFQCTHGVRSSDTRQFFENRPPCDPAKVCVLVNEVHMYNRHQYEEVLNLSVDSCEVDH
AtMLH1 (264) EDMEGCHNSNYVAKKTIL---VLFINDLVECSALKKAIEIQAATLPKASKPEVYMSNLPRHVDN
Consensus (281) F I GFISN H KS FIN R D A L R I VY K PFV L I L E VDIIN

351 420
humPMS2 (336) VIEDRQILQEEKLLAVLKTSLIGMFDSDVNKLNVQQPLLVEGNLIMHAEDLEKPMVEKQDQSPS
AtMLH1 (331) IHEITKEVSLNQEIIIEMIQ-----SEVE-----VALRNDTRTPCEQKVEYIQ
Consensus (351) I P KK I L III MI S IKL A K E

421 490
humPMS2 (406) LRTGEEKVSVISRLREAFSLRHTENKHSHPKTPEPRRSLSQKRGMSSTSGAISDKGVLRPQKEA
AtMLH1 (377) STLTSQSSSPVQKPSG---QKQKVVNKMVRTDSSDEASRLHAFQPKPQLPDKVSSSVVRSS
Consensus (421) K D IS A T P P G A L L K AV

491 560
humPMS2 (476) SSSHGSDPTIRAELEKDSGHGSTSDVSEGFSPDTGSHCSSEYAASSPGDRSCSHSDSQEKAPETDS
AtMLH1 (443) RQRNEKETALSSQOE-----LIA--G-----VDSCHPCLMLETARNCTIYVGMADV
Consensus (491) P D D A V I S G E V DD

561 630
humPMS2 (546) ESDVDCHSNQELGCKFRVLPQPTNLATPNTIRFKKEEISSSDICQKLVTQDMSAQVDVAVKINKKV
AtMLH1 (489) EALQYN-----EHLILAN-----VVNLSEELMYQQTERRFAHFNAIQLSDPAPISLILLALKEEDL
Consensus (561) FA V T SK L N I S S L L L

631 700
humPMS2 (616) VLDFSMSSAKGKQLHHEAQSEGEONYRKRAKCPGENAAAEDELKKEISKTFPAEMIIGQFNEG
AtMLH1 (547) DGNQDKDCKEKAEMNTILLKEKASMLEEYSVHEDSSANLSRLPVILDQYTPDQDRVPSFL--LQCG
Consensus (631) P S L RI L E AE F I N A I S M E I LG

701 770
humPMS2 (686) FIITKLNDIFIVDQHEITDEKYNFEMLQQHTVLOQRLIAPQTLNLTAVNEAVIENLEIFRKNGFVFI
AtMLH1 (615) NDVEWEDKSCFQGVSAIGNFYAMHPPLLPNPSDGIQFYSKRGESSQEKSDLEGVLMEDNLDOLLS
Consensus (701) I E A F G I SA A L NLDI D L

771 840
humPMS2 (756) ENAPVTEAKLISLPTSKNTFGPDQVDDELIFMSDSPGVMCPRSPQMFASRACKRSVMIGTALNTS
AtMLH1 (685) ENAWACE-----ESSIQHVLFPMSRLPKPPASMASNGTFEIVASLEKLYKIFERC-----
Consensus (771) D R WS L L M S VK K K

841 877
humPMS2 (826) EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISQN
AtMLH1 (738) -----
Consensus (841) -----

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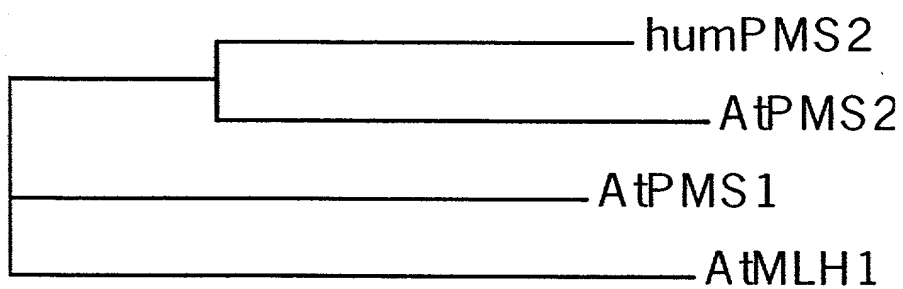
FIG. 3



humPMS2	(1)	MERAESSSTEPAAKIDRKSVQICSGQVVLSTAKELWENSLDAGATNIDLKLKDYGVLDLIEK	70
AtPMS1	(1)	-----MRTKGLPEGVRSMSRSIIIMFDMARVDEELFNSLDAGAKVSIIFGVVSCS-VKTV	
Consensus	(1)	K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D	
humPMS2	(71)	NECCVEENFEGTLKHHTSHIQEADLQVETFGFRGEALSELCAISDVTISCHASAKVETELMFDH	140
AtPMS1	(59)	DESSSRDDLVLGERYASRPHDGTNVEASETFGFRGEALASISDIISLLEVRKAIGRPNSYKVMKG	
Consensus	(71)	G GV D L KH TSK DF L T ETFGFRGEALASI IS L I T G R M	
humPMS2	(140)	NGKIIQKTPYPFP-RCVNSQQESTLEVHHEFERNIKREYAKMVQVLHAYCIISAGI-----	210
AtPMS1	(129)	SKCLHLGIDDDKDSCTATIRDLAYSQVVRHYMSSPKVLESIKKCVPRIALVHNSVFSVLDIESD	
Consensus	(141)	I R GTIVSV LF S PVR K Q KK I L II A I	
humPMS2	(199)	-----RVSCTNQLGQCRQPVVCCGSPSIKESISV	280
AtPMS1	(199)	EELFQTNPSSSAFSLMRDAGTEAVNSLCKVNVTDGLMNSGFECADDWPTDGQCRNRRLQSFPYI	
Consensus	(211)	VS K TG I NG I	
humPMS2	(231)	-----GQKQLQSLIPVQLPSSDSVCEYGCSCSDALHNFYISCFISQCTHVGCRSSTRQF	350
AtPMS1	(269)	LCIACPRRLYESEFEPKTHVEKKWGVLAFLRITANWKKDRIELFDSGADILAKQRQDLIDKI	
Consensus	(281)	F S I F P A E LA L G G D	
humPMS2	(290)	FFINR-----RPCDPAFVCRVLVNEVYHMYNRHOYFVVLNISVSECVDINTPDKRQILE	420
AtPMS1	(339)	RLQGSLSILHFLDADWPPEAMEPAKKLKRSDNHAPCSLLFESADFKQDGYFSPRKDWSPECEVE	
Consensus	(351)	N DPAK H FP D V I L	
humPMS2	(346)	QEEKLLAVLKTSLIGMFDSDVNKLNVSQPLLVVEGNLIKMHADLEKPMVEEDQSPSLFGEEKKDV	490
AtPMS1	(409)	KIQNPKEQGTIVAGFESRTCSLLQSRDIEMTNEFPQVTDLLETSLVADSKCRFLTRCQITFPVNINH	
Consensus	(421)	DS LN I Q D L A L KQ S T	
humPMS2	(416)	SISRLREAFS-----RRTTENKPHSEKTEPRRPLQG	560
AtPMS1	(479)	DFMKDSVDLNFQFQGLKDELVDVSNCTIGKHLRGCSSRVSLTFHEPKSEVEGYESVVEIMINEKQSPRV	
Consensus	(491)	K D L H P P K S	
humPMS2	(450)	KRGMLSSSTSGAISDAGVLRPQKEAVSSSHG--SDPTDPAEKEKDSGHGSVSEGESIPITGSHCSS	630
AtPMS1	(549)	LETREGGSCYCDVYSDRTPDCSLGSSWQDWDFTSCCSSDEGCGIGEDFNIPIITAEISYSEKVGSKK	
Consensus	(561)	S SDK A S P SDRA V T IDS F D	
humPMS2	(518)	EYAASSPDRGSQEHVDSQ-----KAEETDDSFSDVDCHSNQEDTGCKFRVLEQTNLATPNTKRFKKE	700
AtPMS1	(619)	YLLSVNVSSSVTGSFCLSSWSPMYSTSATKWESEYQKGRILEQSLRLGRMDSEFCFSAANNIKFDH	
Consensus	(631)	AA G S S E P SD D K LP P S	
humPMS2	(583)	EILSSSIQKLVTQMSASQVDVVKENK-----VVLDFSMSLAKRIKQLHHEACQSEGENYRK	770
AtPMS1	(689)	EVIPENCSETGIDSFTAIQNTQLDEKCSWGHADDVRIDQYSIRIEKFSYMDGTENNAKRSKRS	
Consensus	(701)	EII D C S LA KI K L SI K QN G Q KK	
humPMS2	(649)	SAKICPGENQ-----	840
AtPMS1	(759)	SAPPFYREKKRFISLCKSDTKPKNSDPSEDDLECLTQPCNASQMHKCSILDDVSYDHIQETEKRLS	
Consensus	(771)	RA	
humPMS2	(659)	-----	910
AtPMS1	(829)	SASDLKASAGCRTVHSETQDEDVHEDFSSEFLDPIKSTTKWRHNCVAVSQVPKESHELHGQDGVFDISSG	
Consensus	(841)		
humPMS2	(659)	-----AASDELKKEISKIMFAEMEIGFNLGFITKLNEDIFVDCHEIDEKYNFEMCOQHTVLQGGQRL	980
AtPMS1	(899)	LLHLRSDSLVPESNRHSLDAKVLQVDDKKYPIVACGTVAVDQSEADERIRLEERTKFINDALLI	
Consensus	(911)	A E L I K D II Q FI I IVDQHA DEK E L I A I	
humPMS2	(724)	IAPQTLNLTAVNEAVIENLIFPKNCFDFVVDENAPVTERAK-----ISLSTSKNNTFGPQ	1050
AtPMS1	(969)	FVLTLKVPEMGYQLQSYSEQIEDWENICMTVEGSTSFKKNMSIIQRKTPITINAVECILGVNLSDV	
Consensus	(981)	L M LL E R GF I A S K L ALP	
humPMS2	(782)	VDELIFMSSESPVMCRSRKQMFASRACKSVICTANTSEMKKLTHMGEMDHPWMPGGRFMR	1120
AtPMS1	(1039)	LLIFLQCASTDSSTIPSLRLVLNKAAGATFDSLLPSECSLIIDGLQTSLSLFCQAGCRFTV	
Consensus	(1051)	DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT	
humPMS2	(852)	HIANGVISQN-----	1164
AtPMS1	(1109)	PLVDKALHKQIAKLSGRQVWHGLQRRITLDRAKSRLDNAKS-	
Consensus	(1121)	I L I N	

FIG. 4





**FIG. 5**





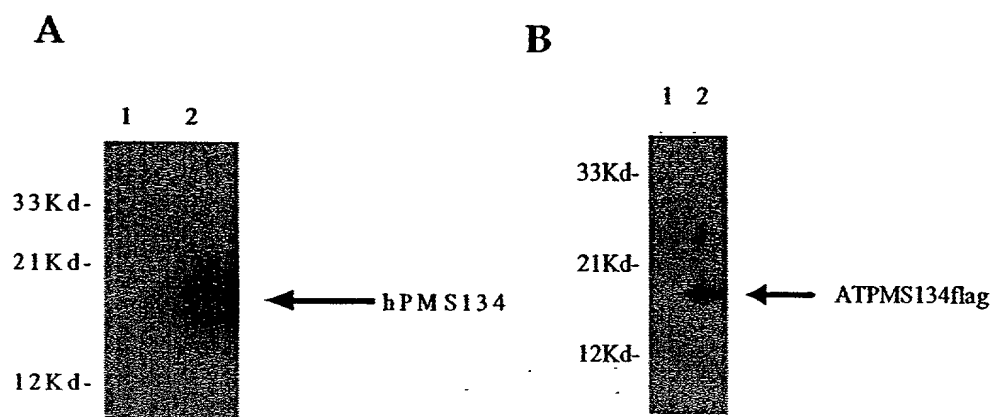


1 70  
 humPMS134 (1) --MERAEESSTEPAKAKKEDKSVQICSGQVHLSSTAVKELVENSIDAGATNIDLKIKDYGVLIET  
 AtPMS134 (1) MQGDSSPPTITSSPLRENNVIERICSGQVHLSSTAVKELVENSIDAGATSEINIRDYGEYFQ  
 Consensus (1) D A S S T A I K P I R I H I C S G Q V I L L S S A V K E L V E N S I D A G A T I D I L K D Y G D V  
 71 140  
 humPMS134 (69) SDNGCGVEEEN-----EGILKHHTSNIQESADLTQVEFGFRGEALSSLCALSDVETISCHA  
 AtPMS134 (71) SDNGCGISPTNKKVCVQILRRTFDVALKHHTSNIQESADLTQVEFGFRGEALSSLCALGNLVEVETRTK  
 Consensus (71) DNGCGI NF D L L K H H T S K I D F D L N L T F G F R G E A L S S L C A L L T I T  
 141  
 humPMS134 (128) SAKYGF  
 AtPMS134 (141) NEPTA  
 Consensus (141) VAT

FIG. 7



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**FIG. 8**



Dominant Negative Effects of *Arabidopsis thaliana* PMS2 homolog

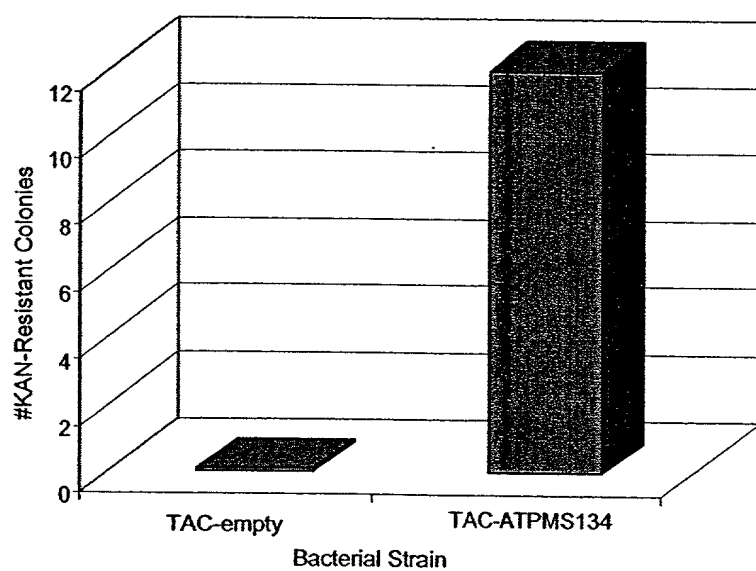


FIG. 9





FIG. 10



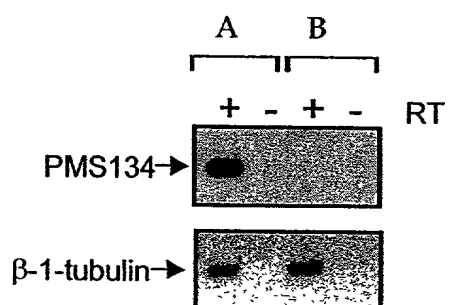


FIG. 11



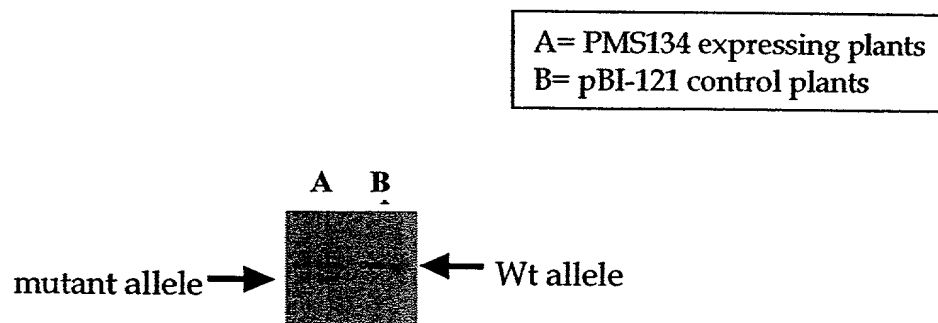
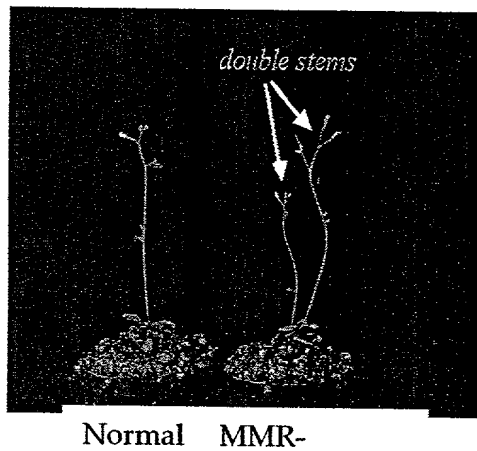


FIG. 12





**FIG. 13**